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## Preface

With the advent of proteomics came the development of technologies, primarily mass spectrometry, which allowed high-throughput identification of proteins in complex mixtures. While the mass spectrometer resides at the heart of proteomics, its ability to characterize biological samples is only as good as the sample preparation and data analysis tools used in any study. Not only has proteomics increased our capacity to identify proteins, it has enabled other characteristics of proteomes to be measured. Of utmost interest has been the development of techniques for measuring posttranslational modifications such as phosphorylation and glycosylation. Since the amount of any specific protein within a cell is important to its function, methods to quantitate protein levels have also been developed. These quantitative methods include both label-free approaches and those that utilize stable isotopes incorporated both during cell growth or added via a chemical reaction once the proteome is extracted from the cell.

The purpose of this book is to provide the student and researcher in the fields of Biochemistry, Biomedicine, Molecular and Cellular Biology, and Bioinformatics a detailed description of many of the different sample preparation and data analysis tools used in proteomics today. The editors are indebted to each of the authors for providing their time and expertise in making this edition an invaluable resource to anyone involved or interested in proteomics.

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